



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.5 [Nov-16-2002]

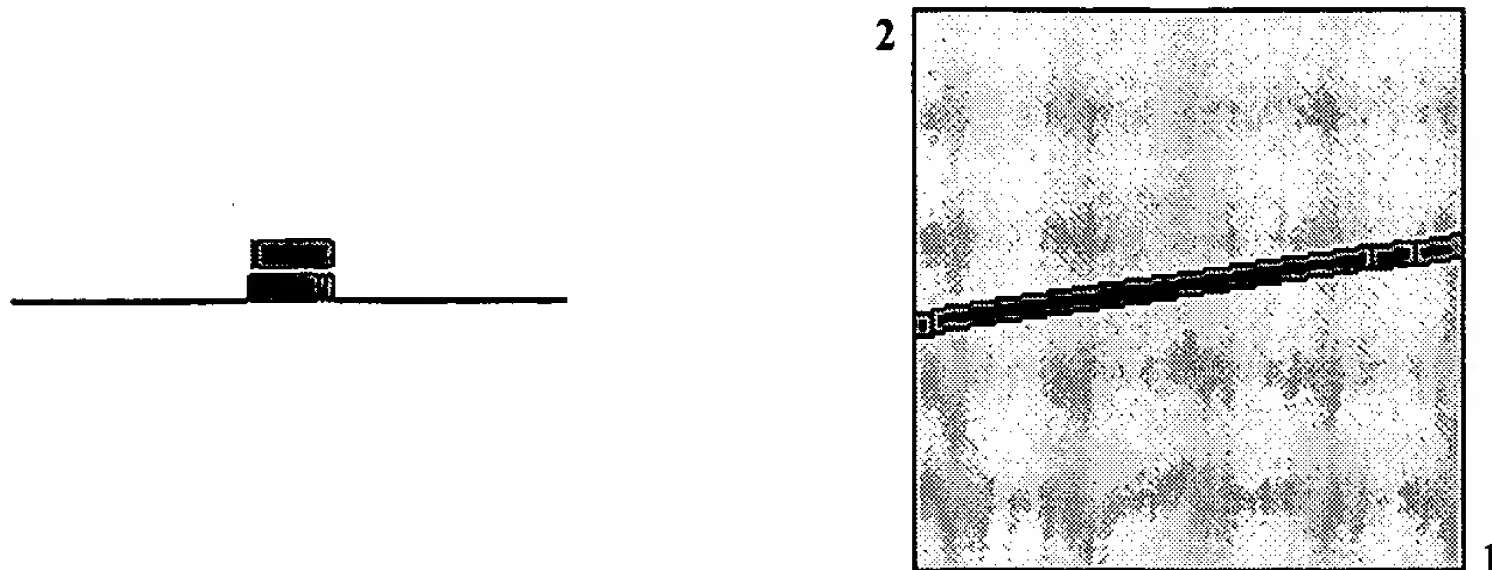
Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: ☒ Filter

Sequence 1 gi_1271750 yz97c02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290978 5' similar to PIR:S01302 S01302 hypothetical protein, 58K ;

Length 386 (1 .. 386)

Sequence 2 gi_16588686

Length 2677 (1 .. 2677)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 694 bits (361), Expect = 0.0
Identities = 383/387 (98%), Gaps = 3/387 (0%)
Strand = Plus / Plus

```
Query:          1      tccaaagctgggaan-tctgtgttccggccatgaacgtcaatgattctgttaccaaacag 59
                  |||
Sbjct:         1164    tccaaagctgggaagctctgtgttccggccatgaacgtcaatgattctgttaccaaacag 1223
S-adenosylhomocysteine hydrolas> 266      S K A G K L C V P A M N V N D S V T K Q

Query:          60      aagtttgataacttgactgctgccgagaatccattttggatggcctgaagaggaccaca 119
                  |||
Sbjct:         1224    aagtttgataacttgactgctgccgagaatccattttggatggcctgaagaggaccaca 1283
S-adenosylhomocysteine hydrolas> 286      K F D N L Y C C R E S I L D G L K R T T

Query:          120      gatgtgatgtttggtgggaacaagtgggtggtgtgtggctatggtgaggtaggcaagggc 179
                  |||
Sbjct:         1284    gatgtgatgtttggtgggaacaagtgggtggtgtgtggctatggtgaggtaggcaagggc 1343
S-adenosylhomocysteine hydrolas> 306      D V M F G G K Q V V V C G Y G E V G K G

Query:          180      tgctgtgctgctctcaaagctcttggagcaattgtctacattaccgaaatcgaccccatc 239
                  |||
Sbjct:         1344    tgctgtgctgctctcaaagctcttggagcaattgtctacattaccgaaatcgaccccatc 1403
S-adenosylhomocysteine hydrolas> 326      C C A A L K A L G A I V Y I T E I D P I

Query:          240      tgtgctctgcaggcctgcatggatgggttcagggtggtaaagctaaatgaagtcacccgg 299
                  |||
Sbjct:         1404    tgtgctctgcaggcctgcatggatgggttcagggtggtaaagctaaatgaagtcacccgg 1463
S-adenosylhomocysteine hydrolas> 346      C A L Q A C M D G F R V V K L N E V I R

Query:          300      caagtcgatgtcgtaataacttngcacaggaaataagaatgtagtgacacgngagcact 359
                  |||
```

Sbjct: 1464 caagtcgatgtcgtaataactt-gcacaggaaataagaatgtagtgacacgg-gagcact 1521
S-adenosylhomocysteine hydrolas> 366 Q V D V V I T C T G N K N V V T R E H

Query: 360 tggatcgcatgaaaaacagttgtatcg 386
|||||
Sbjct: 1522 tggatcgcatgaaaaacagttgtatcg 1548
S-adenosylhomocysteine hydrolas> 385 L D R M K N S C I

CPU time: 0.06 user secs. 0.05 sys. secs 0.11 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 386
length of database: 8,484,804,551
effective HSP length: 24
effective length of query: 362
effective length of database: 8,484,804,527
effective search space: 3071499238774
effective search space used: 3071499238774
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)